

SEQUENCE LISTING

<110> GOKHALE, Rajesh
 TSUJI, Stuart
 KHOSLA, Chaitan
 WU, Nicholas
 CANE, David

<120> METHODS TO MEDIATE POLYKETIDE SYNTHASE
 MODULE EFFECTIVENESS

<130> 300622004601

<140> US 10/506,630
 <141> 2002-03-04

<150> PCT/US03/06910
 <151> 2002-03-04

<150> US 10/091,244
 <151> 2002-03-04

<150> 60/361,758
 <151> 2002-03-04

<160> 41

<170> FastSEQ for Windows Version 4.0

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 <212> DNA
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<220>
 <223> Nhe site upstream of the KS at position 7570

<400> 1
 gctagcgagc cgatc

15

<210> 2
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 <213> Artificial Sequence

<220>
 <223> Nhe site upstream of the KS at position 28710

<400> 2
 gctagcgacc cgatc

15

<210> 3
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chemically synthesized

<221> misc feature
<223> N-terminal linker

<400> 3
Met Thr Asp Ser Glu Lys Val Ala Glu Tyr Leu Arg Arg Ala Thr Leu
1 5 10 15
Asp Leu Arg Ala Ala Arg Gln Arg Ile Arg Glu Leu Glu Ser Asp
20 25 30

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<220>
<223> Primer

<400> 4
actagtaggc tggtcgcggc ctcac 25

<210> 5
<211> 24
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<220>
<223> Primer

<400> 5
gggaattcag gtcctctccc ccgc 24

<210> 6
<211> 23
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<220>
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<400> 6
ccatatggtg gtcgaccggc tcg 23

<210> 7
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<220>
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<400> 7
gaattcctac aggtcctctc cccc 24

<210> 8
<211> 22
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<220>
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 <400> 8
 ccatatgctg cgcgaccggc tg 22

 <210> 9
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 <400> 9
 gaattctcaa tcgccgtcga gctcc 25

 <210> 10
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 <400> 10
 ccatatggtg gtcgaccggc tcg 23

 <210> 11
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 <400> 11
 actagtgagg aaaccggcga ccg 23

 <210> 12
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 <400> 12
 ccatatgctg cgcgaccggc tg 22

 <210> 13
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<400> 13
gaattcttag ccgagctcgg cgtc

24

<210> 14
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<400> 14
ccatatggtg gtcgaccggc tcg

23

<210> 15
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<220>
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<400> 15
gaattcttag aacagcctgt cccgcag

27

<210> 16
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<220>
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<400> 16
ctgctcgaga ggctgttcgc ggcctca

27

<210> 17
<211> 27
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<220>
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<400> 17
cccgtgagc ctacaggtcc tctcccc

27

<210> 18
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<220>
<223> Intra-polypeptide linker

Asp

<210> 23
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<212> PRT
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<220>
<223> Intra-polypeptide linker

<400> 23
Gly Glu Thr Val Ala Gly Ala Pro Ala Thr Pro Val Thr Thr Val Ala
1 5 10 15
Asp Ala Gly

<210> 24
<211> 21
<212> PRT
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<220>
<223> Intra-polypeptide linker

<400> 24
Glu Leu Phe Thr Gly Glu Asn Pro Ala Pro Val Arg Gly Pro Val Ser
1 5 10 15
Ala Val Gly Gln Asp
20

<210> 25
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<220>
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<400> 25
Glu Leu Phe Thr Gly Glu Asn Pro Ala Pro Val Arg Gly Pro Val Ser
1 5 10 15
Val Val Gly Gln Asp
20

<210> 26
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 26
Glu Leu Phe Thr Gly Glu Asn Pro Ala Pro Val Arg Gly Pro Val Ser
1 5 10 15
Ala Gly Gln Asp
20

<210> 27
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 27
Val Thr Asp Ser Glu Lys Val Ala Glu Tyr Leu Arg Arg Ala Thr Leu
1 5 10 15
Asp Leu Arg Ala Ala Arg Gln Arg Ile Arg Glu Leu Glu Ser
20 25 30

<210> 28
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 28
Met Ser Gly Asp Asn Gly Met Thr Glu Glu Lys Leu Arg Arg Tyr Leu
1 5 10 15
Lys Arg Thr Val Thr Glu Leu Asp Ser Val Thr Ala Arg Leu Arg Glu
20 25 30
Val Glu His Arg Ala Gly
35

<210> 29
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 29
Met Ser Ala Pro Asn Glu Gln Ile Val Asp Ala Leu Arg Ala Ser Leu
1 5 10 15
Lys Glu Asn Val Arg Leu Gln Gln Glu Asn Ser Ala Leu Ala Ala Ala
20 25 30
Ala Ala

<210> 30
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 30
Val Ser Ala Ser Tyr Glu Lys Val Val Glu Ala Leu Arg Lys Ser Leu
1 5 10 15

Glu Glu Val Gly Thr Leu Lys Lys Arg Asn Arg Gln Leu Ala Asp Ala
 20 25 30
 Ala Gly

<210> 31
 <211> 33
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-Terminal Inter-polypeptide linker

<400> 31
 Val Ala Asp Glu Gly Gln Leu Arg Asp Tyr Leu Lys Arg Ala Ile Ala
 1 5 10 15
 Asp Ala Arg Asp Ala Arg Thr Arg Leu Arg Glu Val Glu Glu Gln Ala
 20 25 30
 Arg

<210> 32
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-Terminal Inter-polypeptide linker

<400> 32
 Met Ala Thr Asp Glu Lys Leu Leu Lys Tyr Leu Lys Arg Val Thr Ala
 1 5 10 15
 Glu Leu His Ser Leu Arg Lys Gln Gly Ala Arg His Ala Asp
 20 25 30

<210> 33
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-Terminal Inter-polypeptide linker

<400> 33
 Met Arg Glu Asp Gln Leu Leu Asp Ala Leu Arg Lys Ser Val Lys Glu
 1 5 10 15
 Asn Ala Arg Leu Arg Lys Ala Asn Thr Ser Leu Arg Ala Ala Met Asp
 20 25 30

<210> 34
 <211> 33
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-Terminal Inter-polypeptide linker

<400> 34

Met Pro Glu Gln Asp Lys Val Val Glu Tyr Leu Arg Trp Ala Thr Ala
 1 5 10 15
 Glu Leu His Thr Thr Arg Ala Lys Leu Glu Ala Leu Ala Ala Ala Asn
 20 25 30
 Thr

<210> 35
 <211> 388
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Alignment of the EryA SU

<400> 35
 Val Val Phe Val Phe Pro Gly Gln Gly Ala Gln Trp Ala Gly Met Ala
 1 5 10 15
 Gly Glu Leu Ile Gly Glu Ser Arg Val Phe Ala Ala Ala Met Asp Ala
 20 25 30
 Cys Ala Arg Ala Phe Glu Pro Val Thr Asp Trp Thr Leu Ala Gln Val
 35 40 45
 Leu Asp Ser Pro Glu Gln Ser Arg Arg Val Glu Val Val Gln Pro Ala
 50 55 60
 Leu Phe Ala Val Gln Thr Ser Leu Ala Ala Leu Trp Arg Ser Phe Gly
 65 70 75 80
 Val Thr Pro Asp Ala Val Val Gly His Ser Ile Gly Glu Leu Ala Ala
 85 90 95
 Ala His Val Cys Gly Ala Ala Gly Ala Ala Asp Ala Ala Arg Ala Ala
 100 105 110
 Ala Leu Trp Ser Arg Glu Met Ile Pro Ile Val Gly Asn Gly Asp Met
 115 120 125
 Met Ala Val Ala Leu Ser Ala Asp Glu Ile Glu Pro Arg Ile Ala Arg
 130 135 140
 Trp Asp Asp Val Val Leu Ala Gly Val Asn Gly Pro Arg Ser Val Leu
 145 150 155 160
 Leu Thr Gly Ser Pro Glu Pro Val Ala Arg Arg Val Gln Glu Leu Ser
 165 170 175
 Ala Glu Gly Val Arg Ala Gln Val Ile Asn Val Ser Met Ala Ala His
 180 185 190
 Ser Ala Gln Val Asp Asp Ile Ala Glu Gly Met Arg Ser Ala Leu Ala
 195 200 205
 Trp Phe Ala Pro Gly Gly Ser Glu Val Pro Phe Tyr Ala Ser Leu Thr
 210 215 220
 Gly Gly Ala Val Asp Thr Arg Glu Leu Val Ala Asp Tyr Trp Arg Arg
 225 230 235 240
 Ser Phe Arg Leu Pro Val Arg Phe Asp Glu Ala Ile Arg Ser Ala Leu
 245 250 255
 Glu Val Gly Pro Gly Thr Phe Val Glu Ala Ser Pro His Pro Val Ile
 260 265 270
 Ala Ala Ala Leu Gln Gln Thr Leu Asp Ala Glu Gly Ser Ser Ala Ala
 275 280 285
 Val Val Pro Thr Leu Gln Arg Gly Gln Gly Gly Met Arg Arg Phe Leu
 290 295 300
 Leu Ala Ala Ala Gln Ala Phe Thr Gly Gly Val Ala Val Asp Trp Thr
 305 310 315 320
 Ala Ala Tyr Asp Asp Val Gly Pro Asn Pro Ala Leu Gly Arg Glu Ala
 325 330 335
 Asp Ala Glu Ala Thr Phe Arg Glu Leu Gly Leu Asp Ser Val Leu Ala
 340 345 350
 Ala Gln Ile Arg Ala Lys Val Ser Ala Ala Ile Gly Arg Glu Val Asn
 355 360 365

Ile Ala Leu Leu Tyr Asp His Pro Thr Pro Arg Ala Leu Ala Glu Ala
 370 375 380
 Leu Ala Ala Gly
 385

<210> 36
 <211> 1397
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Alignment of the EryA SU

<400> 36
 Ala Ala Pro Gly Glu Pro Val Ala Val Val Ala Met Ala Cys Arg Leu
 1 5 10 15
 Pro Gly Gly Val Ser Thr Pro Glu Glu Phe Trp Glu Leu Leu Ser Glu
 20 25 30
 Gly Arg Asp Ala Val Ala Gly Leu Pro Thr Asp Arg Gly Trp Asp Leu
 35 40 45
 Asp Ser Leu Phe His Pro Asp Pro Thr Arg Ser Gly Thr Ala His Gln
 50 55 60
 Arg Gly Gly Gly Phe Leu Thr Glu Ala Thr Ala Phe Asp Pro Ala Phe
 65 70 75 80
 Phe Gly Met Ser Pro Arg Glu Ala Leu Ala Val Asp Pro Gln Gln Arg
 85 90 95
 Leu Met Leu Glu Leu Ser Trp Glu Val Leu Glu Arg Ala Gly Ile Pro
 100 105 110
 Pro Thr Ser Ile Gln Ala Ser Pro Thr Gly Val Phe Val Gly Leu Ile
 115 120 125
 Pro Gln Glu Tyr Gly Pro Arg Leu Ala Glu Gly Gly Glu Gly Val Glu
 130 135 140
 Gly Tyr Leu Met Thr Gly Thr Thr Thr Ser Val Ala Ser Gly Arg Ile
 145 150 155 160
 Ala Tyr Thr Leu Gly Leu Glu Gly Pro Ala Ile Ser Val Asp Thr Ala
 165 170 175
 Cys Ser Ser Ser Leu Val Ala Val His Leu Ala Cys Gln Ser Leu Arg
 180 185 190
 Arg Gly Glu Ser Ser Ile Ala Met Ala Gly Gly Val Thr Val Met Pro
 195 200 205
 Thr Pro Gly Met Leu Val Asp Phe Ser Arg Met Asn Ser Leu Ala Pro
 210 215 220
 Asp Gly Arg Cys Lys Ala Phe Ser Ala Gly Ala Asn Gly Phe Gly Met
 225 230 235 240
 Ala Glu Gly Ala Gly Met Leu Leu Ile Glu Arg Leu Ser Asp Ala Arg
 245 250 255
 Arg Asn Gly His Pro Val Leu Ala Val Leu Arg Gly Thr Ala Val Asn
 260 265 270
 Ser Asp Gly Ala Ser Asn Gly Leu Ser Ala Pro Asn Gly Arg Ala Gln
 275 280 285
 Val Arg Val Ile Gln Gln Ala Leu Ala Glu Ser Gly Leu Gly Pro Ala
 290 295 300
 Asp Ile Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp
 305 310 315 320
 Pro Ile Glu Ala Arg Ala Leu Phe Glu Ala Tyr Gly Arg Asp Arg Glu
 325 330 335
 Gln Pro Leu His Leu Gly Ser Val Lys Ser Asn Leu Gly His Thr Gln
 340 345 350
 Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met Arg
 355 360 365
 Ala Gly Thr Leu Pro Arg Thr Leu His Ala Ser Glu Arg Ser Lys Glu

370	375	380
Ile Asp Trp Ser Ser Gly Ala Ile Ser Leu Ile Asp Glu Pro Glu Pro		
385	390	395
Trp Pro Ala Gly Ala Arg Pro Arg Arg Ala Gly Val Ser Ser Phe Gly		400
	405	410
Ile Ser Gly Thr Asn Ala His Ala Ile Ile Glu Glu Ala Pro Gln Val		415
	420	425
Val Glu Gly Glu Arg Val Glu Ala Gly Asp Val Val Ala Pro Trp Val		430
	435	440
Leu Ser Ala Ser Ser Ala Glu Gly Leu Arg Ala Gln Ala Ala Arg Leu		445
	450	455
Ala Ala His Leu Arg Glu His Pro Gly Gln Asp Pro Arg Asp Ile Ala		460
	465	470
Tyr Ser Leu Ala Thr Gly Arg Ala Ala Leu Pro His Arg Ala Ala Phe		475
	485	490
Ala Pro Val Asp Glu Ser Ala Ala Leu Arg Val Leu Asp Gly Leu Ala		495
	500	505
Thr Gly Asn Ala Asp Gly Ala Ala Val Gly Thr Ser Arg Ala Gln Gln		510
	515	520
Arg Ala Val Phe Val Trp Ala Ala Val Asp Asp Thr Ser Pro Ala Ala		525
	530	535
Leu Arg Glu Ala Asp Ala Leu Glu Pro His Leu Asp Arg Glu Val Ile		540
	545	550
Pro Phe Leu Arg Ala Glu Ala Ala Arg Arg Glu Gln Asp Ala Ala Leu		555
	565	570
Ser Thr Glu Asp Val Val Met Ala Val Met Val Ser Met Arg Ala His		575
	580	585
Val Glu Ala Ile Gln Ile Cys Ala Ala Leu Ser Leu Asp Asp Ala Ala		590
	595	600
Arg Val Val Ala Leu Arg Ser Arg Val Ile Ala Thr Met Pro Gly Asn		605
	610	615
Lys Gly Ala Ser Ile Ala Ala Pro Ala Gly Glu Val Arg Ala Arg Ile		620
	625	630
Gly Asp Arg Val Glu Ile Ala Gly Arg Ser Val Val Val Ala Asp Ser		635
	645	650
Asp Glu Leu Asp Arg Leu Val Ala Ser Cys Thr Thr Glu Cys Ile Arg		655
	660	665
Ala Lys Arg Leu Ala Asp Tyr Ser Ser Ser His Val Glu Thr Ile Arg		670
	675	680
Asp Ala Leu His Ala Glu Leu Gly Glu Asp Phe His Pro Leu Pro Gly		685
	690	695
Phe Val Pro Phe Phe Thr Val Thr Gly Arg Trp Thr Gln Pro Asp Glu		700
	705	710
Leu Asp Ala Gly Tyr Arg Asn Ile Arg Thr Arg Ala Asp Val Arg Ala		715
	725	730
Leu Ala Glu Gln Tyr Arg Thr Leu Val Ala Ile Leu Thr Ala Ala Ile		735
	740	745
Glu Glu Ile Gly Asp Gly Ser Gly Ala Asp Leu Ser Ala Ile His Ser		750
	755	760
Arg Gly Asp Gly Ser Leu Ala Asp Phe Gly Glu Ala Leu Ser Arg Phe		765
	770	775
Ala Ala Ala Val Asp Trp Glu Ser Val His Leu Gly Thr Gly Ala Arg		780
	785	790
Arg Val Pro Leu Pro Thr Tyr Pro Phe Gln Arg Glu Arg Val Trp Leu		795
	805	810
Glu Pro Lys Pro Val Ala Arg Arg Ser Thr Glu Val Asp Glu Val Ser		815
	820	825
Ala Leu Arg Tyr Arg Ile Glu Trp Arg Pro Thr Gly Ala Gly Glu Pro		830
	835	840
Ala Arg Leu Asp Gly Thr Trp Leu Val Ala Lys Tyr Ala Gly Thr Ala		845
	850	855
Asp Glu Thr Ser Thr Ala Ala Arg Glu Ala Leu Glu Ser Ala Gly Ala		860

865					870					875				880	
Arg	Val	Arg	Glu	Leu	Val	Val	Asp	Ala	Arg	Cys	Gly	Arg	Asp	Glu	Leu
				885					890					895	
Ala	Glu	Arg	Leu	Arg	Ser	Val	Gly	Glu	Val	Ala	Gly	Val	Leu	Ser	Leu
			900					905					910		
Leu	Ala	Val	Asp	Glu	Ala	Glu	Pro	Glu	Glu	Ala	Pro	Leu	Ala	Leu	Ala
		915						920					925		
Ser	Leu	Ala	Asp	Thr	Leu	Ser	Leu	Val	Gln	Ala	Met	Val	Ser	Ala	Glu
	930					935					940				
Leu	Gly	Cys	Pro	Leu	Trp	Thr	Val	Thr	Glu	Ser	Ala	Val	Ala	Thr	Gly
945					950					955					960
Pro	Phe	Glu	Arg	Val	Arg	Asn	Ala	Ala	His	Gly	Ala	Leu	Trp	Gly	Val
				965					970						975
Gly	Arg	Val	Ile	Ala	Leu	Glu	Asn	Pro	Ala	Val	Trp	Gly	Gly	Leu	Val
			980					985					990		
Asp	Val	Pro	Ala	Gly	Ser	Val	Ala	Glu	Leu	Ala	Arg	His	Leu	Ala	Ala
		995						1000					1005		
Val	Val	Ser	Gly	Gly	Ala	Gly	Glu	Asp	Gln	Leu	Ala	Leu	Arg	Ala	Asp
	1010					1015					1020				
Gly	Val	Tyr	Gly	Arg	Arg	Trp	Val	Arg	Ala	Ala	Ala	Pro	Ala	Thr	Asp
1025					1030					1035					1040
Asp	Glu	Trp	Lys	Pro	Thr	Gly	Thr	Val	Leu	Val	Thr	Gly	Gly	Thr	Gly
				1045					1050						1055
Gly	Val	Gly	Gly	Gln	Ile	Ala	Arg	Trp	Ile	Ala	Arg	Pro	Gly	Ala	Pro
			1060					1065						1070	
His	Leu	Leu	Leu	Val	Ser	Arg	Ser	Gly	Pro	Asp	Ala	Asp	Gly	Ala	Gly
	1075						1080					1085			
Glu	Leu	Val	Ala	Glu	Leu	Glu	Ala	Leu	Gly	Ala	Arg	Thr	Thr	Val	Ala
	1090					1095					1100				
Ala	Cys	Asp	Val	Ile	Asp	Arg	Glu	Ser	Val	Arg	Glu	Leu	Leu	Gly	Gly
1105					1110					1115					1120
Ile	Gly	Asp	Asp	Val	Pro	Leu	Ser	Ala	Val	Phe	His	Ala	Ala	Ala	Thr
				1125					1130						1135
Leu	Asp	Asp	Gly	Thr	Val	Asp	Thr	Leu	Thr	Gly	Glu	Arg	Ile	Glu	Arg
			1140					1145					1150		
Ala	Ser	Arg	Ala	Lys	Val	Leu	Gly	Ala	Arg	Asn	Leu	His	Glu	Leu	Thr
	1155						1160					1165			
Arg	Glu	Leu	Asp	Leu	Thr	Ala	His	Val	Leu	Phe	Ser	Ser	Phe	Ala	Ser
	1170					1175					1180				
Ala	Phe	Gly	Ala	Pro	Gly	Leu	Gly	Gly	Tyr	Ala	Pro	Gly	Asn	Ala	Tyr
1185					1190					1195					1200
Leu	Asp	Gly	Leu	Ala	Gln	Gln	Arg	Arg	Ser	Asp	Gly	Leu	Pro	Ala	Thr
				1205					1210						1215
Ala	Val	Ala	Trp	Gly	Thr	Trp	Ala	Gly	Ser	Gly	Met	Ala	Glu	Gly	Ala
			1220					1225					1230		
Val	Ala	Asp	Arg	Phe	Arg	Arg	His	Gly	Val	Ile	Glu	Met	Pro	Pro	Glu
	1235						1240					1245			
Thr	Ala	Cys	Arg	Ala	Leu	Gln	Asn	Ala	Leu	Asp	Arg	Ala	Glu	Val	Cys
	1250					1255					1260				
Pro	Ile	Val	Ile	Asp	Val	Arg	Trp	Asp	Arg	Phe	Leu	Leu	Ala	Tyr	Thr
1265					1270					1275					1280
Ala	Gln	Arg	Pro	Thr	Arg	Leu	Phe	Asp	Glu	Ile	Asp	Asp	Ala	Arg	Arg
				1285					1290						1295
Ala	Ala	Pro	Gln	Ala	Pro	Ala	Glu	Pro	Arg	Val	Gly	Ala	Leu	Ala	Ser
		1300					1305						1310		
Leu	Pro	Ala	Pro	Glu	Arg	Glu	Glu	Ala	Leu	Phe	Glu	Leu	Val	Arg	Ser
	1315						1320					1325			
His	Ala	Ala	Ala	Val	Leu	Gly	His	Ala	Ser	Ala	Glu	Arg	Val	Pro	Ala
	1330					1335					1340				
Asp	Gln	Ala	Ala	Glu	Val	Leu	Ser	Leu	Glu	Asn	Arg	Leu	Gly	Ala	Ala
1345					1350					1355					1360
Thr	Val	Arg	Leu	Pro	Thr	Thr	Thr	Val	Phe	Asp	Asp	Val	Arg	Thr	Leu

	1365		1370		1375
Ala His Leu	Ala Ala Glu Leu Gly	Gly Ala Thr Gly Ala	Glu Gln Ala		
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Ala Pro Ala Thr Thr					
	1395				

<210> 37
 <211> 1114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Alignment of the EryA SU

<400> 37

Ala Pro Val Asp Glu Ile Ile Gly Met Ala Leu Glu Val Asp Ser Glu																	
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Arg Leu Glu Leu Ile Thr Ser Gly Arg Asp Ser Ala Ala Glu Val Asp							20						25				
		20												30			
Val Pro Asp Glu Leu Met Ala Ser Asp Ala Ala Gly Thr Arg Ala His														35			
		35												40			
Asn Phe Met Ala Gly Gly Asp Ala Ala Ile Ser Leu Met Gln Ala Thr														45			
		50												55			
Thr Ala Leu Ser Ile Pro Glu Thr Arg Gly Ser Asp Val Met Ser His														60			
		65												70			
Gln Gly Ala Thr Gly Arg Pro Arg Pro Glu Asp Gly Val Asp Leu Leu														75			
		85												80			
Thr Asn Thr Ala Ser Ala Ile Ala Val Leu Leu Ala Leu Thr Ser Val														85			
		100												90			
Ala Leu Thr Cys Gly Ser Asp Gly Asp Gln Gly Leu Val Ala Val Ser														95			
		115												100			
Ala Gly Glu Val Phe Thr Glu Ser Arg Gln Gly Ala Ser Pro Cys Pro														105			
		130												110			
Ser Asp Glu Asp Gly Leu Gly Ser Ala Phe Val Val Gln Arg Asp Arg														115			
		145												120			
Glu Arg Arg Gly Val Val Ala Ser Val Gln Ser Ser Val Ala Gln Arg														125			
		165												130			
Arg Trp Ala Arg Ala Ile Thr Gly Ala Val Ala Val Arg Val Ala Ser														135			
		180												140			
Leu Ala Thr Lys Ser Gly Ser Ser Gly Val Leu Leu Ser Ile Ala Val														145			
		195												150			
Ala Ile Val Ile Gly Leu Glu Arg Val Val Pro Met Cys Arg Gly Arg														155			
		210												160			
Ser Gly Leu Ile Asp Ser Ser Glu Ile Glu Leu Ala Asp Gly Val Arg														165			
		225												170			
Glu Ser Pro Ala Ala Asp Gly Val Gly Ala Val Val Ile Ala Pro Glu														175			
		245												180			
Pro Glu Pro Val Pro Gln Pro Arg Arg Met Leu Pro Ala Thr Gly Val														185			
		260												190			
Val Val Val Leu Ala Arg Thr Gly Ala Ala Leu Arg Gly Arg Leu Ala														195			
		275												200			
Asp His Leu Ala Ala His Pro Gly Ile Ala Pro Ala Asp Val Ser Trp														205			
		290												210			
Thr Met Arg Ala Gln His Phe Glu Glu Ala Val Leu Ala Ala Asp Thr														215			
		305												220			
Ala Glu Ala Val His Arg Arg Ala Val Asp Ala Val Val Pro Gly Val														225			
		325												230			
Val Thr Gly Ser Ala Ser Asp Gly Gly Ser Val Phe Val Ala Glu Ala														235			
		340												240			
Arg Glu Pro Val Pro Glu Ser Ile Ala Glu Asp Ala Val Leu Ser Glu														245			
		355												250			
														255			
														260			
														265			
														270			
														275			
														280			
														285			
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														365			

Val	Ala	Gly	Arg	Ser	Val	Ser	Glu	Val	Leu	Glu	Pro	Arg	Pro	Asp	Ala	
	370					375					380					
Pro	Ser	Leu	Glu	Asp	Val	Val	Leu	Ala	Val	Met	Val	Arg	Leu	Arg	Ala	
385					390					395					400	
Cys	Ala	Val	Ser	Ile	Gln	Ile	Val	Ala	Ala	Leu	Ser	Leu	Glu	Asp	Gly	
				405					410					415		
Met	Arg	Val	Val	Ala	Arg	Arg	Ser	Arg	Ala	Val	Arg	Ala	Val	Ala	Gly	
			420						425				430			
Arg	Gly	Ser	Leu	Ser	Val	Arg	Gly	Gly	Arg	Ser	Asp	Val	Glu	Lys	Leu	
		435					440					445				
Leu	Ala	Asp	Asp	Ser	Trp	Thr	Gly	Arg	Leu	Glu	Val	Ala	Gly	Asp	Ala	
	450					455					460					
Val	Val	Val	Ala	Asp	Ala	Gln	Ala	Ala	Arg	Glu	Phe	Leu	Glu	Tyr	Cys	
465					470					475					480	
Glu	Gly	Val	Gly	Ile	Arg	Ala	Arg	Ala	Ile	Pro	Asp	Tyr	Ser	Thr	Ala	
				485					490					495		
His	Val	Glu	Pro	Val	Arg	Asp	Glu	Leu	Val	Gln	Ala	Leu	Ala	Gly	Ile	
			500					505					510			
Thr	Pro	Arg	Arg	Ala	Glu	Val	Pro	Phe	Phe	Thr	Leu	Thr	Gly	Asp	Phe	
		515					520					525				
Leu	Asp	Gly	Thr	Glu	Leu	Asp	Ala	Gly	Tyr	Arg	Asn	Ile	His	Pro	Glu	
	530					535					540					
His	Ser	Val	Gln	Ala	Leu	Thr	Asp	Gln	Tyr	Ala	Thr	Ile	Val	Pro	Val	
545					550					555					560	
Leu	Ala	Ser	Ser	Val	Gln	Glu	Thr	Leu	Asp	Asp	Ala	Glu	Ser	Asp	Ala	
				565					570					575		
Ala	Val	Leu	Gly	Thr	Glu	Asp	Ala	Gly	Asp	Ala	Asp	Arg	Phe	Leu	Thr	
			580					585					590			
Ala	Leu	Ala	Asp	His	Thr	Arg	Ala	Val	Asp	Trp	Glu	Ala	Val	Leu	Gly	
		595					600					605				
Arg	Ala	Gly	Leu	Val	Asp	Gly	Gln	Gly	Lys	Phe	Leu	Leu	Pro	Asp	Arg	
	610					615					620					
Thr	Thr	Pro	Arg	Glu	Leu	Asp	Gly	Trp	Phe	Arg	Val	Asp	Thr	Glu	Val	
625					630					635					640	
Pro	Arg	Ser	Glu	Pro	Ala	Ala	Leu	Arg	Gly	Arg	Trp	Val	Val	Val	Pro	
				645					650					655		
Glu	Gly	His	Glu	Glu	Asp	Gly	Trp	Thr	Val	Glu	Val	Arg	Ser	Ala	Leu	
		660						665					670			
Ala	Glu	Ala	Ala	Glu	Pro	Glu	Val	Thr	Arg	Gly	Val	Gly	Gly	Leu	Val	
		675					680					685				
Gly	Asp	Cys	Ala	Gly	Val	Leu	Leu	Ala	Leu	Glu	Gly	Asp	Gly	Ala	Val	
	690					695				700						
Gln	Thr	Leu	Val	Val	Arg	Glu	Leu	Asp	Ala	Glu	Gly	Ile	Asp	Ala	Pro	
705					710					715					720	
Leu	Trp	Thr	Val	Phe	Gly	Asp	Ala	Gly	Ser	Pro	Val	Ala	Arg	Pro	Asp	
				725					730					735		
Gln	Ala	Lys	Leu	Trp	Leu	Gly	Gln	Val	Ala	Ser	Leu	Arg	Gly	Pro	Arg	
			740					745					750			
Trp	Thr	Gly	Leu	Val	Leu	Pro	His	Met	Pro	Asp	Pro	Glu	Leu	Arg	Gly	
		755					760					765				
Arg	Leu	Thr	Val	Leu	Ala	Gly	Ser	Glu	Asp	Gln	Val	Val	Ala	Asp	Ala	
	770					775					780					
Val	Arg	Ala	Arg	Leu	Ser	Pro	Ala	His	Val	Thr	Ala	Thr	Ser	Glu	Tyr	
785					790					795					800	
Ala	Val	Gly	Ile	Val	Gly	Thr	Ala	Gly	Leu	Ala	Glu	Val	Ala	Trp	Ala	
				805					810					815		
Gly	Arg	Ala	Glu	His	Ala	Val	Ser	Arg	Arg	Gly	Pro	Asp	Thr	Glu	Gly	
			820					825					830			
Val	Gly	Asp	Thr	Ala	Glu	Leu	Thr	Asp	Leu	Ala	Arg	Val	Ser	Val	His	
		835					840					845				
Cys	Val	Ser	Ser	Arg	Glu	Pro	Val	Arg	Glu	Ile	Val	His	Gly	Leu	Ile	
	850					855					860					

Glu	Gln	Gly	Asp	Val	Val	Arg	Gly	Val	Val	Ala	Ala	Gly	Leu	Pro	Gln	865	870	875	880
Gln	Val	Ala	Ile	Asn	Asp	Met	Asp	Glu	Ala	Ala	Phe	Asp	Glu	Val	Val				
Ala	Ala	Ala	Gly	Gly	Ala	Val	His	Asp	Leu	Cys	Ser	Asp	Ala	Glu	Leu	885	890	895	
His	Leu	Ile	Phe	Gly	Gly	Val	Trp	Gly	Ser	Ala	Arg	Gln	Gly	Ala	Ala	900	905	910	
Ala	Gly	Asn	Ala	Phe	Asp	Ala	Phe	Arg	His	Arg	Gly	Arg	Leu	Pro	Ala	915	920	925	
Thr	Ser	Val	Ala	Gly	Leu	Ala	Gly	Gly	Met	Thr	Gly	Asp	Glu	Glu	Ala	930	935	940	
Val	Ser	Phe	Leu	Arg	Glu	Arg	Val	Arg	Ala	Met	Pro	Val	Pro	Arg	Leu	945	950	955	960
Ala	Ala	Leu	Asp	Arg	Val	Ala	Ser	Gly	Glu	Thr	Ala	Val	Val	Val	Thr	965	970	975	
Asp	Val	Asp	Trp	Pro	Ala	Phe	Ala	Glu	Ser	Tyr	Thr	Ala	Arg	Pro	Arg	980	985	990	
Pro	Leu	Leu	Asp	Arg	Ile	Val	Thr	Thr	Ala	Pro	Ser	Glu	Arg	Ala	Gly	995	1000	1005	
Glu	Pro	Glu	Thr	Glu	Ser	Leu	Arg	Asp	Arg	Leu	Gly	Leu	Pro	Arg	Ala	1010	1015	1020	
Glu	Arg	Thr	Ala	Glu	Val	Arg	Leu	Val	Arg	Thr	Ser	Thr	Thr	Val	Leu	1025	1030	1035	1040
His	Asp	Asp	Pro	Lys	Ala	Val	Arg	Ala	Thr	Thr	Pro	Lys	Glu	Phe	Leu	1045	1050	1055	
Ala	Val	Arg	Asn	Leu	Leu	Asn	Ala	Ala	Thr	Leu	Arg	Leu	Pro	Ser	Thr	1060	1065	1070	
Leu	Val	Phe	Asp	Asn	Ala	Ser	Ala	Val	Gly	Phe	Leu	Asp	Ala	Glu	Gly	1075	1080	1085	
Thr	Glu	Val	Arg	Gly	Glu	Ala	Pro	Ser	Ala							1090	1095	1100	
																1105	1110		

<210> 38

<211> 1128

<212> PRT

<213> Artificial Sequence

<220>

<223> Alignment of the EryA SU

<400> 38

Glu	Leu	Glu	Ser	Asp	Ile	Ile	Ser	Met	Ala	Leu	Gly	Val	Asn	Thr	Gln	1	5	10	15
Arg	Ile	Glu	Leu	Leu	Arg	Glu	Gly	Gly	Glu	Thr	Leu	Ser	Gly	Phe	Thr	20	25	30	
Asp	Leu	Ala	Arg	Leu	His	His	Pro	Asp	Pro	Asp	Asn	Pro	Gly	Thr	Ser	35	40	45	
Tyr	Val	Asp	Lys	Gly	Phe	Leu	Asp	Asp	Ala	Gly	Ala	Glu	Val	Ser	Ala	50	55	60	
Met	Leu	Ile	Thr	Ser	Leu	Val	Asn	Ile	Asp	His	Ser	Arg	Gly	Thr	Ala	65	70	75	80
Leu	Val	Ala	Lys	Phe	Gly	Gly	Glu	Asp	Thr	Ala	Ala	Ala	Glu	Asp	Val	85	90	95	
Glu	Ser	Val	Thr	Val	Ala	Pro	Ala	Ala	Ile	Ser	Thr	Met	Leu	Ser	Ile	100	105	110	
Ser	Ser	Val	Ala	Leu	Ile	Val	Glu	Ser	Lys	Gly	Glu	Ser	Ser	Met	Val	115	120	125	
Val	Ala	Ala	Ala	Thr	Gly	Val	Phe	Val	Asp	Ser	Arg	Gln	Arg	Ala	Ala	130	135	140	
Ala	Ser	Ala	Gly	Ala	Gly	Asp	Gly	Phe	Ser	Val	Thr	Leu	Val	Leu	Glu				

145					150					155					160
Arg	Glu	Arg	Asn	His	Glu	Ala	Val	Val	Arg	Ser	Ile	Gln	Ser	Ser	Pro
				165					170					175	
Ala	Arg	Arg	Gln	Leu	Glu	Ser	Cys	Leu	Glu	Pro	Gly	Val	Asp	Ala	Ala
			180					185					190		
Ile	Ala	Asn	Leu	Asp	Thr	Arg	Asp	Asp	Ala	Asp	Arg	Leu	Trp	Leu	Ser
		195					200					205			
Ile	Thr	Val	Thr	Leu	Val	Val	Ala	Leu	Arg	Asn	Glu	Leu	Ala	Thr	His
	210					215					220				
Val	Glu	Pro	Thr	Pro	His	Val	Asp	Ser	Ser	Gly	Val	Ala	Leu	Leu	Ala
225					230					235					240
Gly	Asn	Gln	Pro	Arg	Arg	Gly	Glu	Arg	Thr	Arg	Ala	Ile	Val	Val	Glu
				245					250					255	
Ala	Glu	Arg	Glu	His	Arg	Glu	Thr	Thr	Ala	His	Asp	Gly	Arg	Pro	Val
			260					265					270		
Leu	Val	Val	Ala	Arg	Thr	Thr	Ala	Ala	Leu	Arg	Ala	Gln	Ile	Ala	Glu
	275						280					285			
Leu	Leu	Glu	Arg	Pro	Asp	Ala	Asp	Leu	Ala	Gly	Val	Gly	Leu	Gly	Leu
290						295					300				
Thr	Thr	Ala	Arg	His	Glu	His	Ala	Val	Val	Ala	Ser	Thr	Arg	Glu	Glu
305					310					315					320
Ala	Val	Arg	Gly	Arg	Glu	Ile	Ala	Ala	Ala	Thr	Ala	Asp	Ala	Val	Val
				325					330					335	
Glu	Gly	Val	Thr	Glu	Val	Asp	Gly	Arg	Asn	Val	Val	Phe	Leu	Ser	Ala
			340				345					350			
Gly	Ala	Glu	Ser	Ser	Ser	Pro	Gly	Lys	Ile	Arg	Ala	Asp	Glu	Ser	Met
	355						360					365			
Ala	Pro	Met	Gln	Asp	Trp	Lys	Val	Ser	Asp	Val	Leu	Arg	Gln	Ala	Pro
	370					375					380				
Gly	Ala	Pro	Gly	Leu	Asp	Asp	Val	Val	Leu	Val	Met	Val	Glu	Leu	Arg
385					390					395					400
Ser	Tyr	Val	Glu	Ala	Val	Gln	Ile	His	Ala	Ala	Leu	Thr	Leu	Glu	Asp
				405					410					415	
Ala	Ala	Lys	Ile	Val	Val	Gly	Arg	Ser	Arg	Ile	Met	Arg	Ser	Leu	Ser
			420						425				430		
Gly	Glu	Gly	Gly	Ala	Ala	Val	Ala	Leu	Gly	Glu	Ala	Ala	Val	Arg	Glu
		435					440					445			
Arg	Leu	Arg	Pro	Trp	Gln	Asp	Arg	Leu	Ser	Val	Ala	Gly	Arg	Ser	Val
	450					455					460				
Val	Val	Ser	Glu	Pro	Gly	Ala	Leu	Arg	Ala	Phe	Ser	Glu	Asp	Cys	Ala
465					470					475					480
Ala	Glu	Gly	Ile	Arg	Val	Arg	Asp	Ile	Asp	Asp	Tyr	Ser	Ser	Pro	Gln
				485					490					495	
Ile	Glu	Arg	Val	Arg	Glu	Glu	Leu	Leu	Glu	Thr	Thr	Gly	Asp	Ile	Ala
			500				505						510		
Pro	Arg	Pro	Ala	Arg	Val	Pro	Phe	His	Thr	Val	Glu	Ser	Arg	Ser	Met
	515						520					525			
Asp	Gly	Thr	Glu	Leu	Asp	Ala	Arg	Tyr	Arg	Asn	Ile	Glu	Thr	Arg	Ala
	530					535					540				
Asp	Val	Thr	Arg	Leu	Ala	Glu	Ser	Tyr	Asp	Ala	Ile	Val	Pro	Val	Val
545					550					555					560
Val	Gln	Ala	Val	Glu	Glu	Gln	Val	Glu	Glu	Ala	Asp	Gly	Ala	Glu	Asp
				565					570					575	
Ala	Val	Val	Val	Gly	Ser	His	Asp	Gly	Gly	Asp	Leu	Ser	Ala	Phe	Leu
			580					585					590		
Arg	Ser	Met	Ala	Thr	His	Val	Ser	Asp	Ile	Arg	Trp	Asp	Val	Ala	Leu
		595					600					605			
Pro	Gly	Ala	Ala	Pro	Phe	Ala	Thr	Gln	Arg	Lys	Tyr	Leu	Gln	Pro	Ala
	610					615					620				
Ala	Pro	Ala	Ala	Ala	Ser	Glu	Leu	Ala	Arg	Val	Ser	Thr	Pro	Ile	Glu
625					630					635					640
Lys	Pro	Glu	Ser	Gly	Asn	Leu	Asp	Gly	Asp	Trp	Val	Val	Thr	Pro	Leu

				645					650					655			
Ile	Ser	Pro	Glu	Trp	Thr	Glu	Met	Leu	Cys	Glu	Ala	Ile	Asn	Ala	Asn		
			660					665					670				
Gly	Arg	Ala	Leu	Arg	Cys	Glu	Val	Asp	Thr	Ser	Ala	Ser	Arg	Thr	Glu		
		675						680					685				
Met	Ala	Gln	Ala	Val	Ala	Gln	Ala	Gly	Thr	Gly	Phe	Arg	Gly	Leu	Leu		
	690					695					700						
Leu	Ser	Ser	Asp	Glu	Ser	Ala	Cys	Arg	Pro	Gly	Val	Pro	Ala	Gly	Ala		
705				710						715					720		
Val	Gly	Leu	Leu	Thr	Val	Gln	Ala	Leu	Gly	Asp	Ala	Gly	Val	Asp	Ala		
				725					730					735			
Pro	Val	Trp	Cys	Leu	Gln	Gly	Arg	Thr	Pro	Ala	Asp	Asp	Asp	Leu	Ala		
			740					745					750				
Arg	Pro	Ala	Gln	Thr	Thr	Ala	His	Phe	Ala	Gln	Val	Ala	Gly	Leu	Leu		
		755					760					765					
Pro	Gly	Arg	Trp	Gly	Gly	Val	Val	Leu	Pro	Glu	Ser	Val	Asp	Asp	Ala		
	770					775				780							
Ala	Leu	Arg	Leu	Leu	Val	Val	Leu	Arg	Gly	Gly	Gly	Arg	Ala	Glu	Asp		
785					790					795					800		
His	Leu	Val	Asp	Gly	Arg	Leu	His	Gly	Arg	Val	Val	Arg	Ala	Ser	Leu		
			805						810					815			
Pro	Gln	Ser	Gly	Ser	Arg	Ser	Trp	Thr	His	Val	Val	Ala	Ala	Ser	Pro		
			820					825					830				
Val	Asp	Gln	Ile	Val	Trp	Ala	Asp	Arg	Ala	Glu	Arg	Val	Ala	Gly	Ala		
		835					840						845				
Cys	Pro	Gly	Asp	Asp	Leu	Ala	Ala	Val	Glu	Glu	Ala	Ala	Ser	Ala	Val		
	850					855					860						
Val	Cys	Gln	Ala	Ala	Ala	Leu	Arg	Glu	Ala	Leu	Gly	Asp	Glu	Pro	Val		
865					870					875					880		
Thr	Ala	Leu	Val	Ala	Gly	Thr	Leu	Thr	Asn	Phe	Gly	Ser	Ile	Ser	Glu		
				885					890					895			
Val	Ala	Pro	Glu	Glu	Phe	Ala	Glu	Thr	Ile	Ala	Ala	Thr	Ala	Leu	Leu		
		900						905					910				
Ala	Val	Asp	Val	Leu	Gly	Asp	Arg	Ala	Val	Glu	Arg	His	Val	Tyr	Cys		
		915					920					925					
Val	Gly	Ile	Trp	Gly	Gly	Ala	Gly	Met	Ala	Ala	Ala	Ala	Gly	Ser	Ala		
	930					935					940						
Tyr	Asp	Ala	Leu	Glu	His	His	Ala	Arg	Arg	Ser	Cys	Thr	Ser	Val	Ala		
945					950					955					960		
Thr	Pro	Leu	Pro	Gly	Gly	Ala	Val	Asp	Asp	Gly	Tyr	Leu	Arg	Glu	Arg		
			965					970						975			
Leu	Arg	Ser	Leu	Ser	Ala	Asp	Arg	Met	Arg	Thr	Trp	Glu	Arg	Val	Ala		
			980					985					990				
Ala	Gly	Pro	Val	Ser	Val	Ala	Val	Ala	Asp	Val	Asp	Trp	Pro	Val	Leu		
		995					1000					1005					
Ser	Glu	Gly	Phe	Ala	Thr	Arg	Pro	Thr	Ala	Leu	Phe	Ala	Glu	Leu	Ala		
	1010					1015					1020						
Gly	Arg	Gly	Gly	Gln	Ala	Glu	Ala	Glu	Pro	Asp	Ser	Gly	Pro	Thr	Gly		
1025					1030					1035					1040		
Glu	Pro	Ala	Gln	Arg	Leu	Gly	Leu	Ser	Pro	Asp	Glu	Gln	Gln	Glu	Asn		
			1045						1050					1055			
Leu	Glu	Leu	Val	Ala	Asn	Ala	Val	Glu	Val	Leu	His	Glu	Ser	Ala	Ala		
			1060					1065					1070				
Glu	Ile	Asn	Val	Arg	Arg	Ala	Ser	Glu	Leu	Leu	Asn	Met	Ala	Lys	Arg		
	1075					1080						1085					
Leu	Ser	Ala	Ser	Thr	Leu	Arg	Leu	Pro	Ala	Ser	Leu	Val	Phe	Asp	Thr		
	1090					1095					1100						
Val	Thr	Ala	Leu	Gln	His	Leu	Arg	Ala	Arg	Val	Gly	Asp	Ala	Asp	Gln		
1105					1110					1115					1120		
Ala	Ala	Val	Arg	Val	Val	Gly	Ala										
				1125													

<210> 39
 <211> 1224
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Alignment of the EryA SU

<400> 39
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 Gln Leu Arg Val Leu Ala Glu Gly Ala Asn Leu Thr Thr Gly Phe Ala
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 Asp Ile Gly Arg Leu Tyr His Pro Asp Pro Asp Asn Pro Gly Thr Ser
 35 40 45
 Tyr Val Asp Lys Gly Pro Leu Thr Asp Ala Asp Pro Gly Ile Thr Leu
 50 55 60
 Met Leu Met Thr Ala Ala Val Arg Ile Asp Asp Ala Arg Gly Thr Asp
 65 70 75 80
 Val Met Asn Gly Gln Ser Met Gln Leu Leu Ala Gly Glu Ala Glu Arg
 85 90 95
 Val Asp Gln Gly Ile Asn Ser Ala Ser Leu Ile Ala Thr Phe Trp Ala
 100 105 110
 Leu Thr Ser Val Gly Ile Ile Met Gln Ala Arg Gly Glu Cys Ser Leu
 115 120 125
 Leu Ala Val Thr Ser Asp Tyr Thr Phe Val Asp Ser Thr Gln Arg Gly
 130 135 140
 Ala Ser Cys Ala Ser Ala Arg Asp Ala Leu Ser Val Ala Ala Leu Val
 145 150 155 160
 Glu Pro Arg Ala Asn His Gln Ala Val Leu Arg Ser Val Gln Ala Asn
 165 170 175
 Pro Ser Glu Arg Gln Leu Ala Ala Ser Val Pro Ala Ala Val Asp Val
 180 185 190
 Glu Ile Ala Gly Ile Ala Thr Gln Asp Asp Arg Leu Arg Leu Thr Ile
 195 200 205
 Thr Ala Ala Ile Val Val Ala Met Arg His Met Leu Arg Ser His Ala
 210 215 220
 Asp Leu Ser Pro His Ile Asp Glu Ser Ala Val Glu Val Ile Arg Glu
 225 230 235 240
 Glu Val Pro Pro Ala Gly Glu Arg Pro Gly Ser Val Val Val Glu Ala
 245 250 255
 Ala Glu Gln Glu Ala Ala Arg Thr Glu Arg Gly Pro Leu Phe Val Leu
 260 265 270
 Gly Arg Ser Glu Ala Val Val Ala Arg Ala Leu Ala Glu His Leu Arg
 275 280 285
 Asp Thr Pro Glu Leu Gly Leu Thr Asp Ala Ala Trp Thr Leu Thr Gly
 290 295 300
 Ala Arg Phe Asp Val Ala Val Gly Asp Asp Arg Ala Gly Val Cys Ala
 305 310 315 320
 Glu Asp Ala Leu Glu Arg Pro Ser Ala Asp Ala Val Ala Pro Val Thr
 325 330 335
 Ser Ala Pro Arg Lys Pro Val Leu Val Ala Val Ala Arg Asp Glu Ser
 340 345 350
 Ser Glu Glu Ser Met Ser Arg Ala Glu Ala Leu Ser Pro His Thr Asp
 355 360 365
 Trp Lys Leu Leu Asp Val Val Arg Gly Asp Gly Gly Pro Asp Pro His
 370 375 380
 Glu Asp Ile Val Leu Ser Ile Met Val Glu Leu Arg Ala His Val Thr
 385 390 395 400
 Ala Val Gln Ile His Ala Ala Leu Ser Leu Glu Ala Ala Ala Lys Val
 405 410 415

Val	Ala	Leu	Arg	Ser	Gln	Val	Leu	Arg	Glu	Leu	Asp	Asp	Gln	Gly	Gly	
			420					425					430			
Val	Ser	Val	Gly	Ala	Ser	Arg	Asp	Glu	Leu	Glu	Thr	Val	Leu	Ala	Arg	
		435					440					445				
Trp	Asp	Gly	Arg	Val	Ala	Val	Ala	Gly	Gly	Thr	Ser	Val	Val	Ala	Pro	
	450					455					460					
Thr	Ala	Glu	Leu	Asp	Glu	Phe	Phe	Ala	Glu	Ala	Glu	Ala	Arg	Glu	Met	
465					470					475					480	
Lys	Pro	Arg	Arg	Ile	Ala	Arg	Tyr	Ser	Ser	Pro	Glu	Val	Ala	Arg	Ile	
				485					490						495	
Glu	Asp	Arg	Ile	Ala	Ala	Glu	Leu	Gly	Thr	Ile	Thr	Ala	Val	Arg	Gly	
			500					505					510			
Ser	Val	Pro	Leu	His	Thr	Val	Thr	Gly	Glu	Val	Ile	Asp	Thr	Ser	Ala	
	515						520					525				
Met	Asp	Ala	Ser	Tyr	Arg	Asn	Ile	Arg	Pro	Leu	Glu	Gln	Val	Arg	Gly	
	530					535					540					
Leu	Val	Glu	Gln	Phe	Asp	Thr	Val	Val	Pro	Val	Leu	Leu	Met	Ala	Val	
545					550					555					560	
Glu	Glu	Thr	Ala	Glu	His	Ala	Gly	Ala	Glu	Val	Thr	Cys	Val	Pro	Thr	
				565					570					575		
Arg	Glu	Gln	Ser	Gly	Pro	His	Glu	Phe	Leu	Arg	Asn	Leu	Leu	Arg	His	
			580					585				590				
Val	His	Gly	Ala	Asp	Leu	Arg	Pro	Ala	Val	Ala	Gly	Gly	Arg	Pro	Ala	
	595						600					605				
Glu	Thr	Glu	His	Gln	Phe	Pro	Arg	Pro	His	Arg	Pro	Ala	Asp	Val	Ser	
	610					615					620					
Ala	Leu	Tyr	Gly	Leu	Ala	Glu	Gln	Gly	Glu	Tyr	Gly	Pro	Ser	Phe	Gln	
625					630					635					640	
Ala	Leu	Arg	Ala	Ala	Arg	Lys	Asp	Asp	Ser	Val	Tyr	Ala	Glu	Val	Ser	
				645					650					655		
Ile	Ala	Ala	Asp	Glu	Glu	Gly	Tyr	Ala	Phe	His	Pro	Val	Leu	Asp	Ala	
			660					665					670			
Val	Ala	Gln	Thr	Leu	Ser	Leu	Gly	Ala	Leu	Gly	Glu	Pro	Gly	Gly	Gly	
	675						680					685				
Lys	Leu	Pro	Phe	Ala	Trp	Asn	Thr	Val	Thr	Leu	His	Ala	Ser	Ala	Thr	
	690					695					700					
Ser	Val	Arg	Val	Val	Ala	Thr	Pro	Ala	Gly	Ala	Asp	Ala	Met	Ala	Leu	
705					710					715					720	
Arg	Val	Thr	Asp	Pro	Ala	Gly	His	Leu	Val	Ala	Thr	Asp	Leu	Val	Val	
				725					730					735		
Arg	Ser	Thr	Gly	Glu	Lys	Trp	Glu	Gln	Pro	Glu	Pro	Arg	Gly	Gly	Glu	
			740					745					750			
Gly	Glu	Leu	His	Ala	Asp	Trp	Gly	Arg	Leu	Ala	Glu	Pro	Gly	Ser	Thr	
	755						760					765				
Gly	Arg	Val	Val	Ala	Ala	Asp	Ala	Ser	Asp	Leu	Asp	Ala	Val	Leu	Arg	
	770					775					780					
Ser	Gly	Glu	Pro	Glu	Pro	Asp	Ala	Val	Leu	Val	Arg	Tyr	Glu	Pro	Glu	
785					790					795					800	
Gly	Asp	Asp	Pro	Arg	Ala	Ala	Arg	His	Gly	Val	Leu	Trp	Ala	Ala		
				805				810					815			
Ala	Leu	Val	Arg	Arg	Trp	Leu	Glu	Gln	Glu	Glu	Leu	Pro	Gly	Ala	Thr	
			820					825					830			
Leu	Val	Ile	Ala	Ser	Gly	Thr	Val	Ser	Asp	Asp	Asp	Ser	Val	Pro	Glu	
	835						840					845				
Pro	Gly	Ala	Ala	Ala	Met	Trp	Val	Ile	Arg	Cys	Ala	Gln	Ala	Ser	Pro	
	850					855					860					
Asp	Arg	Phe	Val	Leu	Leu	Thr	Asp	Ala	Glu	Pro	Gly	Met	Leu	Pro	Val	
865					870					875					880	
Pro	Asp	Asn	Pro	Gln	Leu	Leu	Gly	Asp	Asp	Val	Phe	Val	Pro	Leu	Ser	
				885					890					895		
Pro	Leu	Ala	Pro	Ser	Ala	Thr	Gln	Pro	Ala	Pro	Val	Asp	Asp	Val	Ile	
			900					905					910			

Gly	Thr	Gly	Thr	Leu	Arg	Leu	Leu	Ala	His	Val	Thr	His	Glu	Val	Arg
	915						920					925			
His	Leu	Val	Ser	Arg	Arg	Gly	Ala	Asp	Ala	Pro	Gly	Ser	Asp	Glu	Arg
	930					935					940				
Ala	Glu	Ile	Glu	Asp	Ile	Ala	Ser	Ala	Glu	Ile	Ala	Cys	Thr	Ala	Asp
945					950					955					960
Arg	Asp	Ala	Leu	Ser	Ala	Leu	Leu	Asp	Gly	Leu	Pro	Arg	Pro	Leu	Thr
				965					970						975
Gly	Val	Val	Ala	Ala	Gly	Val	Leu	Ala	Asp	Gly	Leu	Val	Thr	Ser	Ile
			980						985						990
Asp	Glu	Pro	Ala	Val	Glu	Gln	Val	Leu	Arg	Ala	Val	Asp	Ala	Ala	Trp
	995						1000					1005			
Asn	His	Leu	Thr	Ala	Asn	Thr	Gly	Leu	Ser	Phe	His	Val	Leu	Phe	Ala
	1010					1015					1020				
Ser	Val	Leu	Ala	Gly	Pro	Gly	Gln	Gly	Val	Ala	Ala	Ala	Asn	Glu	Ser
1025					1030					1035					1040
Asn	Ala	Leu	Ala	Leu	Arg	Thr	Arg	Leu	Pro	Ala	Lys	Ala	Leu	Gly	Gly
				1045					1050						1055
Leu	Gln	Ala	Ser	Glu	Met	Thr	Ser	Gly	Leu	Gly	Asp	Arg	Ile	Ala	Arg
			1060					1065							1070
Thr	Val	Ala	Ala	Leu	Pro	Thr	Glu	Arg	Leu	Ala	Leu	Phe	Asp	Ser	Ala
	1075						1080					1085			
Arg	Arg	Gly	Gly	Glu	Val	Val	Phe	Pro	Leu	Ser	Ile	Asn	Arg	Ser	Ala
	1090					1095					1100				
Leu	Arg	Arg	Glu	Phe	Val	Pro	Glu	Val	Leu	Arg	Gly	Met	Val	Arg	Ala
1105					1110				1115						1120
Lys	Leu	Arg	Ala	Ala	Gly	Gln	Ala	Glu	Ala	Ala	Gly	Pro	Asn	Val	Val
			1125					1130							1135
Asp	Arg	Leu	Gly	Arg	Ser	Glu	Ser	Asp	Gln	Val	Ala	Gly	Ala	Glu	Leu
		1140					1145						1150		
Val	Arg	Ser	His	Ala	Ala	Val	Ser	Tyr	Gly	Ser	Ala	Asp	Gln	Leu	Pro
	1155					1160						1165			
Glu	Arg	Lys	Ala	Lys	Asp	Phe	Leu	Ala	Val	Glu	Asn	Arg	Leu	Gly	Thr
	1170				1175					1180					
Ala	Thr	Val	Arg	Leu	Pro	Ser	Thr	Leu	Val	Phe	Asp	Thr	Pro	Leu	Ala
1185					1190				1195						1200
Val	Glu	His	Leu	Arg	Asp	Arg	Phe	Ala	Ala	Ser	Pro	Ala	Val	Asp	Ile
			1205					1210							1215
Gly	Asp	Arg	Leu	Asp	Glu	Leu	Glu								
			1220												

<210> 40

<211> 1118

<212> PRT

<213> Artificial Sequence

<220>

<223> Alignment of the EryA SU

<400> 40

His	Arg	Ala	Gly	Glu	Ile	Ile	Gly	Met	Ala	Phe	Asp	Val	Asp	Ser	Glu
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Ser	Phe	Glu	Phe	Val	Ser	Gly	Gly	Gly	Asp	Ala	Ile	Ala	Glu	Ala	Ala
			20					25					30		
Glu	Pro	Asp	Pro	Asp	Ala	Arg	Leu	Gly	Met	Leu	Ala	Ala	Gly	Asp	Ala
		35					40				45				
Gly	Ile	Ser	Leu	Met	Ile	Met	Ile	Ser	Ala	Leu	Arg	His	Asp	Val	Ser
	50					55					60				
Arg	Gly	Ser	Ala	Ile	Val	Gly	Thr	Val	Asp	Gly	Pro	Arg	Pro	Asp	Glu
65					70				75						80
Ala	Pro	Asp	Glu	Val	Leu	Val	Gly	Thr	Thr	Ala	Ser	Ser	Ala	Val	Ala

				85					90				95				
Cys	Leu	Leu	Ala	Met	Thr	Gly	Thr	Ala	Leu	Ile	Met	Glu	Ser	Arg	Asp		
			100					105					110				
Glu	Cys	Gly	Leu	Ile	Ala	Val	Thr	Ser	Ser	Gly	Ala	Phe	Thr	Glu	Arg		
		115					120					125					
Ser	Gln	Gly	Gly	Ala	Ala	Cys	Pro	Ser	Lys	Ala	Asp	Gly	Leu	Ala	Ala		
		130				135					140						
Gly	Val	Leu	Val	Gln	Arg	Ala	Arg	Glu	Arg	Pro	Ala	Val	Leu	Arg	Ser		
145					150					155					160		
Val	Gln	Thr	Ser	Pro	Ala	Gln	Arg	Arg	Leu	Glu	Asn	Ala	Val	Arg	Ala		
				165					170						175		
Gly	Val	Asp	Tyr	Arg	Ile	Val	His	Leu	Ser	Thr	Ala	Glu	Asp	Pro	Asp		
			180					185					190				
Asp	Leu	Trp	Ile	Ser	Ile	Thr	Val	Ala	Met	Ala	Val	Ala	Leu	Arg	His		
		195					200					205					
Glu	Met	Arg	Thr	His	Phe	Asp	Pro	Ser	Pro	Gln	Ile	Glu	Asp	Leu	Ala		
	210					215					220						
Val	Ser	Val	Val	Ser	Gln	Ala	Arg	Ser	Pro	Ala	Gly	Glu	Arg	Pro	Gly		
225					230					235					240		
Ser	Ile	Val	Val	Glu	Ala	Glu	Ala	Asp	Glu	Pro	Glu	Pro	Ala	Pro	Asp		
				245				250						255			
Ser	Gly	Pro	Val	Leu	Val	Leu	Gly	Arg	Asp	Glu	Gln	Ala	Met	Arg	Gly		
			260					265					270				
Arg	Leu	Ala	Asp	His	Leu	Ala	Arg	Glu	Pro	Arg	Asn	Ser	Leu	Arg	Asp		
		275					280					285					
Thr	Gly	Phe	Thr	Leu	Thr	Arg	Ser	Ala	Trp	Glu	His	Val	Val	Val	Gly		
	290					295					300						
Asp	Arg	Asp	Asp	Ala	Leu	Ala	Gly	Arg	Ala	Val	Asp	Arg	Ile	Ala	Asp		
305					310					315					320		
Arg	Thr	Ala	Thr	Gly	Gln	Ala	Arg	Thr	Arg	Arg	Gly	Val	Ala	Met	Val		
				325				330						335			
Ala	Gln	Ala	Arg	Asp	Arg	Glu	Ser	Gln	Asp	Ser	Ile	Arg	Asp	Glu	Arg		
			340					345					350				
Ala	Leu	Ala	Pro	His	Val	Asp	Trp	Ser	Leu	Thr	Asp	Leu	Leu	Ser	Gly		
		355					360					365					
Ala	Arg	Pro	Leu	Asp	Asp	Val	Ala	Leu	Ala	Val	Met	Val	Ala	Leu	Arg		
	370					375				380							
Ser	His	Val	Glu	Ala	Val	Gln	Ile	His	Ala	Ala	Leu	Thr	Leu	Glu	Asp		
385					390					395					400		
Ala	Ala	Lys	Leu	Val	Ala	Val	Arg	Ser	Arg	Val	Leu	Ala	Arg	Leu	Gly		
			405					410						415			
Gly	Gln	Gly	Gly	Ala	Ser	Phe	Gly	Leu	Gly	Thr	Glu	Gln	Ala	Ala	Glu		
			420					425					430				
Arg	Ile	Gly	Arg	Phe	Ala	Gly	Ala	Leu	Ser	Ile	Ser	Gly	Arg	Ser	Val		
		435				440						445					
Val	Val	Ala	Glu	Ser	Gly	Pro	Leu	Asp	Glu	Leu	Ile	Ala	Glu	Cys	Glu		
	450					455					460						
Ala	Glu	Gly	Ile	Thr	Ala	Arg	Arg	Ile	Pro	Asp	Tyr	Ser	Ser	Pro	Gln		
465					470					475					480		
Val	Glu	Ser	Ile	Arg	Glu	Glu	Leu	Leu	Thr	Glu	Leu	Ala	Gly	Ile	Ser		
				485				490						495			
Pro	Val	Ser	Ala	Asp	Val	Ala	Leu	Tyr	Thr	Thr	Thr	Gly	Gln	Pro	Ile		
			500					505					510				
Asp	Thr	Ala	Thr	Met	Asp	Thr	Ala	Tyr	Ala	Asn	Leu	Glu	Gln	Arg	Gln		
		515					520					525					
Asp	Thr	Arg	Gln	Leu	Ala	Glu	Ala	Phe	Asp	Ala	Val	Val	Pro	Val	Leu		
		530				535					540						
Thr	Val	Gly	Ile	Glu	Ala	Thr	Leu	Asp	Ser	Ala	Leu	Pro	Ala	Asp	Ala		
545					550					555					560		
Gly	Ala	Cys	Val	Val	Gly	Thr	Arg	Asp	Arg	Gly	Gly	Leu	Ala	Asp	Phe		
				565				570						575			
His	Thr	Ala	Leu	Gly	Glu	Tyr	Ala	Gln	Glu	Val	Asp	Trp	Ser	Pro	Ala		

			580					585					590			
Phe	Ala	Asp	Ala	Arg	Pro	Val	Glu	Val	Gln	Arg	Gln	Tyr	Leu	Pro	Ile	
		595					600					605				
Pro	Thr	Gly	Gly	Arg	Ala	Arg	Glu	Asp	Asp	Asp	Trp	Arg	Gln	Val	Val	
		610				615					620					
Arg	Glu	Ala	Glu	Trp	Glu	Ser	Ala	Ser	Leu	Ala	Gly	Arg	Val	Leu	Val	
625					630					635					640	
Thr	Gly	Pro	Gly	Val	Pro	Ser	Glu	Leu	Ser	Asp	Ala	Ile	Arg	Ser	Gly	
				645					650					655		
Leu	Glu	Gln	Ser	Ala	Thr	Val	Leu	Thr	Cys	Asp	Val	Glu	Ser	Arg	Ser	
			660					665					670			
Thr	Ile	Gly	Thr	Ala	Leu	Glu	Ala	Ala	Asp	Thr	Asp	Ala	Leu	Ser	Thr	
		675					680					685				
Val	Leu	Leu	Ser	Arg	Asp	Gly	Glu	Ala	Val	Asp	Pro	Ser	Leu	Asp	Ala	
		690				695					700					
Leu	Ala	Val	Gln	Ala	Leu	Gly	Ala	Ala	Gly	Val	Glu	Ala	Pro	Leu	Trp	
705					710					715					720	
Val	Leu	Arg	Asn	Gln	Val	Ala	Asp	Gly	Glu	Leu	Val	Asp	Pro	Ala	Gln	
			725						730					735		
Ala	Met	Val	Gly	Leu	Gly	Arg	Val	Val	Gly	Ile	Gln	Pro	Gly	Arg	Trp	
			740					745					750			
Gly	Gly	Leu	Val	Leu	Val	Asp	Ala	Asp	Ala	Ala	Ser	Ile	Arg	Ser	Leu	
		755					760					765				
Ala	Val	Leu	Ala	Asp	Pro	Arg	Gly	Glu	Glu	Gln	Val	Ile	Ala	Asp	Gly	
		770				775					780					
Ile	Lys	Val	Ala	Leu	Val	Pro	Ala	Pro	Ala	Arg	Ala	Ala	Arg	Thr	Arg	
785					790					795					800	
Trp	Ser	Arg	Val	Val	Gly	Thr	Gly	Gly	Ile	Ala	His	Val	Ala	Trp	Ala	
				805					810					815		
Arg	Ser	Ala	Glu	His	Val	Leu	Gly	Arg	Arg	Gly	Ala	Asp	Ala	Pro	Gly	
			820					825					830			
Ala	Ser	Glu	Arg	Glu	Glu	Leu	Thr	Ala	Leu	Thr	Gly	Val	Thr	Ile	Ala	
		835					840					845				
Cys	Val	Ala	Asp	Arg	Ala	Arg	Leu	Glu	Ala	Val	Leu	Ala	Ala	Glu	Arg	
		850				855					860					
Ala	Glu	Gly	Arg	Thr	Val	Ser	Ala	Val	Met	Ala	Ala	Gly	Val	Ser	Thr	
865					870					875					880	
Ser	Thr	Pro	Leu	Asp	Asp	Leu	Thr	Glu	Ala	Glu	Phe	Thr	Glu	Ile	Ala	
				885					890					895		
Asp	Val	Val	Arg	Gly	Thr	Val	Asn	Asp	Leu	Cys	Pro	Asp	Leu	Asp	Ala	
			900					905					910			
His	Val	Leu	Phe	Asn	Gly	Val	Trp	Gly	Ser	Pro	Gly	Leu	Ala	Ser	Ala	
		915					920					925				
Ala	Ala	Asn	Ala	Phe	Asp	Gly	Phe	Arg	Arg	Arg	Ser	Glu	Ala	Pro	Val	

1075	1080	1085
Phe Asp Thr Ile Thr Arg	Leu Asp His Tyr Leu	Glu Arg Val Gly Ala
1090	1095	1100
Ala Glu Ala Glu Gln Ala	Pro Ala Leu Val Arg	Glu Val Pro
1105	1110	1115

<210> 41
 <211> 1099
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Alignment of the EryA SU

<400> 41

Lys	Asp	Ala	Asp	Asp	Ile	Ile	Gly	Met	Ala	Phe	Gly	Val	His	Asn	Gly
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Glu	Leu	Glu	Phe	Ile	Val	Gly	Arg	Gly	Asp	Ala	Val	Thr	Glu	Met	Thr
			20					25					30		
Asp	Leu	Asp	Ala	Leu	Phe	Asp	Pro	Asp	Pro	Gln	Arg	His	Gly	Thr	Ser
			35				40					45			
Tyr	Ser	Arg	His	Ala	Phe	Leu	Asp	Gly	Ala	Asp	Ala	Ala	Ile	Ser	Leu
			50			55					60				
Met	Gln	Val	Thr	Thr	Leu	Phe	Asn	Ile	Asp	His	Ser	Arg	Gly	Ser	Asp
65					70				75					80	
Leu	Ala	Ala	Tyr	Gln	Gly	Gly	Gln	Asp	Ala	Val	Val	Pro	Glu	Asp	Ser
				85					90					95	
Glu	Leu	Leu	Thr	Asn	Ser	Ser	Ala	Val	Val	Ala	Val	Leu	Leu	Ala	Val
			100					105					110		
Thr	Ser	Val	Ala	Leu	Ser	Cys	Gly	Ser	Asp	Gly	Asp	Cys	Gly	Leu	Val
			115				120					125			
Ala	Val	Ser	Ala	Gly	Glu	Val	Phe	Thr	Glu	Ser	Arg	Gln	Gly	Gly	Ala
			130				135					140			
Val	Cys	Ala	Ser	Ala	Glu	Asp	Gly	Phe	Ala	Val	Ala	Val	Val	Leu	Gln
145					150				155					160	
Arg	Asp	Arg	Ala	Arg	Gln	Gly	Val	Val	Ala	Ser	Leu	Gln	Ala	Ser	Val
				165					170					175	
Ala	Gln	Arg	Lys	Trp	Ala	Arg	Ala	Ile	Thr	Gly	Ala	Val	Ala	Val	Arg
			180					185					190		
Val	Ala	Ser	Leu	Ala	Thr	Lys	Ser	Gly	Ser	Ser	Gly	Val	Leu	Leu	Ser
			195				200					205			
Ile	Ala	Val	Ala	Ile	Val	Val	Gly	Leu	Asn	Arg	Leu	Val	Pro	Met	Cys
			210			215					220				
Arg	Gly	Arg	Ser	Pro	Leu	Ile	Glu	Ser	Ser	Gly	Val	Glu	Leu	Ala	Glu
225					230					235				240	
Ala	Val	Ser	Pro	Pro	Pro	Ala	Ala	Asp	Gly	Val	Gly	Ala	Val	Val	Ile
				245					250					255	
Ala	Pro	Glu	Pro	Glu	Pro	Leu	Pro	Glu	Pro	Gly	Pro	Val	Gly	Val	Leu
			260					265					270		
Ala	Ala	Ala	Asn	Ser	Val	Val	Leu	Leu	Ala	Arg	Thr	Glu	Thr	Ala	Leu
			275				280					285			
Ala	Arg	Leu	Leu	Glu	Ser	Ala	Val	Asp	Asp	Ser	Val	Pro	Leu	Thr	Ala
			290			295					300				
Leu	Ala	Ser	Ala	Leu	Thr	Gly	Ala	His	Leu	Pro	Arg	Ala	Leu	Ile	Ala
					310					315				320	
Gly	Asp	His	Glu	Gln	Leu	Arg	Gly	Gln	Arg	Ala	Val	Glu	Val	Ala	Ala
				325					330					335	
Pro	Gly	Ala	Thr	Thr	Gly	Thr	Ala	Ser	Ala	Gly	Gly	Val	Val	Phe	Val
			340					345					350		
Ala	Glu	Ala	Arg	Gly	Ser	Val	Pro	Glu	Ser	Ile	Ala	Glu	Asp	Ala	Val
			355				360					365			

Leu	Ser	Glu	Val	Ala	Gly	Phe	Ser	Ala	Ser	Glu	Val	Leu	Glu	Gln	Arg		
370						375					380						
Pro	Asp	Ala	Pro	Ser	Leu	Glu	Asp	Val	Val	Leu	Ser	Val	Met	Val	Arg		
385					390					395					400		
Leu	Gly	Ala	Cys	Val	Ser	Ser	Ile	Gln	Ile	Val	Ala	Val	Leu	Ser	Leu		
				405					410					415			
Glu	Asp	Gly	Val	Arg	Val	Val	Ala	Leu	Arg	Ala	Lys	Ala	Leu	Arg	Ala		
			420					425					430				
Leu	Ala	Gly	Arg	Gly	Gly	Val	Ser	Leu	Ala	Ala	Pro	Gly	Glu	Arg	Ala		
		435					440					445					
Arg	Ala	Leu	Ile	Ala	Pro	Trp	Glu	Asp	Arg	Ile	Ser	Val	Ala	Ser	Ser		
450						455					460						
Ser	Val	Val	Val	Ser	Asp	Pro	Glu	Ala	Leu	Ala	Glu	Leu	Val	Ala	Arg		
465					470					475					480		
Cys	Glu	Asp	Glu	Gly	Val	Arg	Ala	Lys	Thr	Leu	Pro	Asp	Tyr	Ser	Ser		
				485					490					495			
Arg	His	Val	Glu	Glu	Ile	Arg	Glu	Thr	Ile	Leu	Ala	Asp	Leu	Asp	Gly		
			500					505					510				
Ile	Ser	Ala	Arg	Arg	Ala	Ala	Ile	Pro	Leu	Tyr	Thr	Leu	His	Gly	Glu		
		515					520					525					
Arg	Arg	Asp	Gly	Ala	Asp	Met	Gly	Pro	Arg	Tyr	Asp	Asn	Leu	Ser	Gln		
530					535						540						
Arg	Asp	Glu	Val	Ser	Ala	Ala	Val	Ala	Asp	His	Ala	Thr	Val	Met	Pro		
545					550					555					560		
Val	Ile	Thr	Ala	Ala	Val	Gln	Glu	Ile	Ala	Ala	Asp	Ala	Val	Ala	Ile		
				565					570					575			
Gly	Ser	His	Asp	Thr	Ala	Glu	Glu	His	Ile	Ile	Ala	Glu	Leu	Ala	Arg		
			580					585				590					
His	Val	His	Ala	Val	Asp	Trp	Arg	Asx	Val	Phe	Pro	Ala	Ala	Pro	Pro		
		595					600					605					
Val	Ala	Asn	Glu	Pro	Gln	Tyr	Leu	Ala	Pro	Glu	Val	Ser	Gln	Leu	Ala		
610					615						620						
Asp	Ser	Arg	Arg	Val	Asp	Arg	Pro	Leu	Ala	Thr	Thr	Pro	Val	Asp	Leu		
625					630					635					640		
Glu	Gly	Gly	Phe	Val	His	Gly	Ser	Ala	Pro	Glu	Ser	Leu	Thr	Ser	Ala		
			645					650						655			
Val	Glu	Lys	Ala	Gly	Arg	Val	Val	Pro	Val	Ala	Ser	Ala	Asp	Arg	Glu		
			660					665					670				
Ala	Ser	Ala	Ala	Leu	Arg	Glu	Val	Pro	Gly	Glu	Val	Ala	Gly	Leu	Val		
		675				680						685					
His	Thr	Gly	Ala	Ala	Thr	His	Leu	Ala	His	Gln	Ser	Leu	Gly	Glu	Ala		
		690				695					700						
Gly	Val	Arg	Ala	Pro	Leu	Trp	Leu	Val	Ser	Arg	Ala	Leu	Gly	Glu	Ser		
705					710					715					720		
Glu	Pro	Val	Asp	Pro	Glu	Gln	Ala	Met	Val	Trp	Leu	Gly	Arg	Val	Met		
			725						730					735			
Gly	Leu	Thr	Pro	Glu	Arg	Trp	Gly	Gly	Leu	Val	Leu	Pro	Ala	Glu	Pro		
			740				745						750				
Ala	Pro	Gly	Asp	Gly	Glu	Ala	Phe	Val	Cys	Leu	Gly	Ala	Asp	Gly	His		
		755					760					765					
Glu	Asp	Gln	Val	Ile	Asp	His	Ala	Arg	Tyr	Gly	Arg	Leu	Val	Arg	Ala		
		770				775					780						
Pro	Leu	Gly	Thr	Arg	Glu	Ser	Ser	Trp	Glu	Ala	Ala	Val	Gly	Thr	Gly		
785					790					795					800		
Ala	Leu	Gly	His	Val	Ala	His	Ala	Arg	Cys	Val	Glu	Asp	Val	Val	Ser		
			805						810					815			
Arg	Arg	Gly	Val	Asp	Ala	Pro	Gly	Ala	Ala	Glu	Glu	Ala	Glu	Leu	Val		
			820				825						830				
Ala	Ile	Ala	Lys	Thr	Thr	Ile	Thr	Cys	Val	Ala	Asp	Arg	Glu	Gln	Leu		
		835					840					845					
Ser	Lys	Leu	Leu	Glu	Glu	Leu	Arg	Gly	Gln	Gly	Arg	Pro	Val	Arg	Thr		
850						855					860						

Val	Val	Thr	Ala	Gly	Val	Pro	Glu	Ser	Arg	Pro	Leu	His	Glu	Ile	Gly
865					870					875					880
Glu	Leu	Glu	Ser	Val	Cys	Ala	Ala	Val	Thr	Gly	Ala	Arg	Leu	Asp	Leu
				885					890						895
Cys	Pro	Asp	Ala	Glu	Thr	His	Val	Leu	Phe	Gly	Gly	Val	Trp	Gly	Ser
			900					905					910		
Ala	Asn	Leu	Gly	Ala	Ser	Ala	Ala	Asn	Ala	Tyr	Asp	Ala	Leu	His	Arg
		915					920					925			
Arg	Ala	Glu	Arg	Ala	Ala	Thr	Ser	Val	Ala	Gly	Ala	Gly	Glu	Gly	Met
	930					935					940				
Ala	Thr	Gly	Asp	Leu	Glu	Gly	Leu	Thr	Arg	Arg	Leu	Arg	Pro	Met	Ala
945					950					955					960
Pro	Glu	Arg	Ile	Arg	Ala	Leu	His	Gln	Ala	Asp	Asn	Gly	Asp	Thr	Cys
				965					970						975
Val	Ser	Ile	Ala	Asp	Val	Asp	Trp	Glu	Ala	Phe	Ala	Val	Gly	Phe	Thr
			980					985					990		
Ala	Arg	Pro	Arg	Pro	Leu	Leu	Asp	Glu	Leu	Val	Thr	Pro	Ala	Val	Gly
		995					1000						1005		
Ala	Val	Pro	Ala	Val	Gln	Ala	Pro	Ala	Arg	Glu	Met	Thr	Ser	Gln	Glu
	1010					1015					1020				
Leu	Glu	Phe	Thr	His	Ser	His	Val	Ala	Ile	Leu	His	Ser	Ser	Pro	Asp
1025					1030					1035					1040
Ala	Val	Gly	Gln	Asp	Gln	Pro	Thr	Glu	Phe	Leu	Thr	Val	Gly	Asn	Gln
				1045					1050						1055
Leu	Gln	Gln	Ala	Thr	Leu	Ala	Leu	Pro	Ala	Thr	Leu	Val	Phe	Glu	Thr
			1060					1065					1070		
Val	Arg	Arg	Leu	Asp	His	Ile	Gly	Gln	Gln	Asp	Ser	Gly	Thr	Pro	Ala
		1075					1080					1085			
Arg	Glu	Ala	Ser	Ser	Ala	Leu	Arg	Asp	Gly	Tyr					
	1090						1095								